RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/831,686_

Source: _PCT/09_

Date Processed by STIC: _8/29/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
        Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/831,686

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                            prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                            ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                            each n or Xaa can only represent a single residue. Please present the maximum number of each
                            residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                            previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                            the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                            Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            (i) ~~SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)~~
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            This sequence is intentionally skipped

                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
    (NEW RULES)   <210> sequence id number
                            <400> sequence id number
                            000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                            In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                            is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                            Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                            "Unknown." Please explain source of genetic material in <220> to <223> section.
                            (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                            listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
                            any value not specifically a nucleotide.

PCT

RAW SEQUENCE LISTING   DATE: 08/27/2003
PATENT APPLICATION: US/09/831,686   TIME: 09:49:06

            Input Set : A:\sequence listing.txt
            Output Set: N:\CRF4\08272003\I831686.raw

        3 <110> APPLICANT: Stephen Alister Locarnini, et al
W--> 4 <120> TITLE OF INVENTION: Biological compositions, components thereof and uses
therefor
        6 <130> FILE REFERENCE: 43232-1
        8 <140> CURRENT APPLICATION NUMBER: US 09/831,686
C--> 9 <141> CURRENT FILING DATE: 2003-04-10
       11 <150> PRIOR APPLICATION NUMBER: EP 99957236.5
       12 <151> PRIOR FILING DATE: 1999-11-10
       14 <150> PRIOR APPLICATION NUMBER: PCT/AU99/00993
       15 <151> PRIOR FILING DATE: 1999-11-10
       17 <160> NUMBER OF SEQ ID NOS: 16
       19 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

     1213 <210> SEQ ID NO: 16   Does Not Comply
     1214 <211> LENGTH: 426   Corrected Diskette Needed
     1215 <212> TYPE: DNA
     1216 <213> ORGANISM: HBV
     1218 <400> SEQUENCE: 16
     1219 atcctgctgc tatgcctcat cttcttgttg gttcttctgg actatcaagg tatgttgccc   60
     1220 gtttgtcctc taattccagg atcatcaacc accagcacgg gaccatgcaa gacctgcaca   120
     1221 actcctgctc aaggaacctc tatgtttccc tcatgttgct gtacaaaacc tatggatgga   180
     1222 aactgcacct gtattcccat cccatcatct tgggctttcg caaaatacct atgggagtgg   240
     1223 gcctcagtcc gtttctcttg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg   300
     1224 ctttcccca ctgtctggct ttcagttata tggatgatgt ggtattgggg gccaagtctg   360
     1225 tacaacatct tgagtccctt tatgccgctg ttaccaattt tcttttgtct ttgggtatac   420
     1226 atttaa   426
W--> 1230 ??
W--> 1232 ??
W--> 1233 (..continued)
W--> 1235 (continued...)
E--> 1243 ns

delete

See pp 2-3, 10 for more error

```
<210>  1
<211>  226
<212>  PRT
<213>  synthetic
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invalid response - see item 10 on Error Summary Sheet

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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<222>  (2)..(2)
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<220>
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<222>  (3)..(3)
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I/e is at location 25

→) what about Xaa at location 27?

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<220>
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1               5                   10                  15
Ala Xaa Xaa Phe Xaa Leu Thr Xaa Ile Xaa Xaa Ile Pro Xaa Ser Leu
            20                  25                  30
Xaa Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Xaa Xaa Xaa Xaa Cys
        35                  40                  45
Xaa Gly Xaa Asn Xaa Gln Ser Xaa Xaa Ser Xaa His Xaa Pro Xaa Xaa
    50                  55                  60
Cys Pro Pro Xaa Cys Xaa Gly Tyr Arg Trp Met Cys Leu Xaa Arg Phe
65                  70                  75                  80
Ile Ile Phe Leu Xaa Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
            85                  90                  95
Leu Leu Asp Xaa Gln Gly Met Leu Xaa Val Cys Pro Leu Xaa Pro Xaa
            100                 105                 110
Xaa Xaa Thr Thr Ser Xaa Xaa Xaa Cys Xaa Thr Cys Xaa Xaa Xaa Xaa
        115                 120                 125
Gln Gly Xaa Ser Xaa Xaa Pro Xaa Xaa Cys Cys Xaa Lys Pro Xaa Xaa
    130                 135                 140
Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Xaa Trp Ala Xaa Xaa Xaa
145                 150                 155                 160
Xaa Leu Trp Glu Xaa Xaa Ser Xaa Arg Xaa Ser Trp Leu Xaa Leu Leu
            165                 170                 175
Xaa Xaa Phe Val Gln Xaa Xaa Xaa Xaa Leu Xaa Pro Xaa Val Trp Xaa
        180                 185                 190
Xaa Xaa Ile Trp Xaa Xaa Trp Xaa Trp Xaa Pro Xaa Xaa Xaa Xaa Ile
        195                 200                 205
Xaa Xaa Pro Phe Xaa Pro Leu Leu Pro Ile Phe Xaa Xaa Leu Xaa Xaa
    210                 215                 220
Xaa Ile
225
```

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\08272003\I831686.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:1; Xaa Pos. 2,3,4,5,8,10,13,18,19,21,24,26,27,30,33,44,45,46,47,49,51
Seq#:1; Xaa Pos. 53,56,57,59,61,63,64,68,70,78,85,100,105,110,112,113,114
Seq#:1; Xaa Pos. 118,119,120,122,125,126,127,128,131,133,134,136,137,140
Seq#:1; Xaa Pos. 143,144,155,158,159,160,161,165,166,168,170,174,177,178
Seq#:1; Xaa Pos. 182,183,184,185,187,189,192,193,194,197,198,200,202,204
Seq#:1; Xaa Pos. 205,206,207,209,210,213,220,221,223,224,225
Seq#:2; Xaa Pos. 48,54,55,56
Seq#:3; N Pos. 3,10,11,15,21,27,45,48,59,62,65,76,86,96,134,153,164,182,203
Seq#:3; N Pos. 208,220,222,225,228,243,249,254
Seq#:4; Xaa Pos. 2,49,52,53,55,56,65,69,75,195,209,211,222
Seq#:16; N Pos. 427

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF4\08272003\I831686.raw**

```
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:32
M:341 Repeated in SeqNo=2
L:945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:957 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:962 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:967 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:972 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:977 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:982 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:987 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:992 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:997 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:1002 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:1007 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:1012 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:1230 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1232 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1233 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1235 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1243 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:1243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1243 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:428 SEQ:16
L:1243 M:112 C: (48) String data converted to lower case,
L:1243 M:252 E: No. of Seq. differs, <211> LENGTH:Input:426 Found:428 SEQ:16
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